

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Su, Michael Shin-San
Fox, Ted
Wilson, Keith Phillip
Germann, Ursula A.
- (ii) TITLE OF INVENTION: Methods For Designing Inhibitors of
Serine/Thereonine Kinases and Tyrosine Kinase
- 10 (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Fish & Neave
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: US
(F) ZIP: 10020
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 25 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 30 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Haley, James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: VPI 97-104
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 596-9000
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35 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 360 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
1 5 10 15

	Ile	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln	Asn	Leu	Ser	Pro	Val	Gly	Ser
				20					25					30		
	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala	Phe	Asp	Thr	Lys	Thr	Gly	Leu
			35					40					45			
5	Arg	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Ile	Ile	His
		50					55					60				
	Ala	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His	Met	Lys	His
	65					70					75					80
10	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Arg	Ser	Leu
					85					90					95	
	Glu	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val	Thr	His	Leu	Met	Gly	Ala	Asp
				100					105					110		
	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys	Leu	Thr	Asp	Asp	His	Val	Gln
			115					120					125			
15	Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala
		130					135					140				
	Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Ala	Val	Asn	Glu
	145					150					155					160
20	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Thr	Asp
					165					170					175	
	Asp	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu
				180					185					190		
	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser
			195					200					205			
25	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Thr	Gly	Arg	Thr	Leu	Phe	Pro
		210					215					220				
	Gly	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys	Leu	Ile	Leu	Arg	Leu	Val	Gly
	225					230					235					240
30	Thr	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys	Ile	Ser	Ser	Glu	Ser	Ala	Arg
					245					250					255	
	Asn	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met	Pro	Lys	Met	Asn	Phe	Ala	Asn
				260					265					270		
	Val	Phe	Ile	Gly	Ala	Asn	Pro	Leu	Ala	Val	Asp	Leu	Leu	Glu	Lys	Met
			275					280					285			
35	Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile	Thr	Ala	Ala	Gln</			

Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro
340 345 350

(2) INFORMATION FOR SEQ ID NO:2:

(ii) MOLECULE TYPE: protein

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15      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 103..104
          (D) OTHER INFORMATION: /note= "amino acid 103 is
isoleucine or leucine"

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20      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 105..106
          (D) OTHER INFORMATION: /product= "OTHER"
      /note= "amino acid 105 is glutamine, threonine or alanine"

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25 (ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 106..107
(D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 106 is aspartic acid or histidine"

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30      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 109..110
          (D) OTHER INFORMATION: /product= "OTHER"
      /note= "amino acid 109 is glutamic acid or glycine"

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35      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 110..111
          (D) OTHER INFORMATION: /product= "OTHER"
      /note= "amino acid 110 is threonine or alanine"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Ala Ala Ala Ala Ala Ala Gly Ala Gly Pro Glu Met Val Arg Gly
1 5 10 15
Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly
20 25 30

	Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Val Asn Lys	35	40	45
	Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr	50	55	60
5	Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His	65	70	75
	Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu	85	90	95
10	Gln Met Lys Asp Val Tyr Xaa Val Xaa Xaa Leu Met Xaa Xaa Asp Leu	100	105	110
	Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr	115	120	125
	Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn	130	135	140
15	Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Thr Thr	145	150	155
	Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro	165	170	175
20	Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp	180	185	190
	Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser	195	200	205
	Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn	210	215	220
25	Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile	225	230	235
	Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile	245	250	255
30	Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu Pro His Lys Asn Lys	260	265	270
	Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp Ser Lys Ala Leu Asp	275	280	285
	Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His Lys Arg Ile Glu Val	290	295	300
35	Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser	305	310	315
	Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp	325	330	335

000490 642490

Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala
340 345 350

Arg Phe Gln Pro Gly Tyr Arg Ser
355 360

5 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 422 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- 15 (A) NAME/KEY: Region
(B) LOCATION: 146..147
(D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 146 is methionine, threonine or alanine"

(ix) FEATURE:

- 20 (A) NAME/KEY: Region
(B) LOCATION: 150..151
(D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 150 is aspartic acid or glycine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25 Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val
1 5 10 15
Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr
20 25 30
Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe
35 40 45
30 Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr
50 55 60
Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala
65 70 75 80
35 Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser
85 90 95
Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu
100 105 110
Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn
115 120 125
40 Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu
130 135 140

	Val	Xaa	Glu	Leu	Met	Xaa	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	145	150	155	160
	Leu	Asp	His	Glu	Arg	Met	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	165	170	175	
5	Ile	Lys	His	Leu	His	Ser	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	180	185	190	
	Ser	Asn	Ile	Val	Val	Lys	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	195	200	205	
10	Gly	Leu	Ala	Arg	Thr	Ala	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	210	215	220	
	Val	Thr	Arg	Tyr	Tyr	Arg	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	225	230	235	240
	Lys	Glu	Asn	Val	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	245	250	255	
15	Val	Arg	His	Lys	Ile	Leu	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	260	265	270	
	Asn	Lys	Val	Ile	Glu	Gln	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	275	280	285	
20	Lys	Leu	Gln	Pro	Thr	Val	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	290	295	300	
	Ala	Gly	Leu	Thr	Phe	Pro	Lys	Leu	Phe	Pro	Asp	Ser	Leu	Phe	Pro	Ala	305	310	315	320
	Asp	Ser	Glu	His	Asn	Lys	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	325	330	335	
25	Ser	Lys	Met	Leu	Val	Ile	Asp	Pro	Ala	Lys	Arg	Ile	Ser	Val	Asp	Asp	340	345	350	
	Ala	Leu	Gln	His	Pro	Tyr	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Val	355	360	365	
30	Glu	Ala	Pro	Pro	Pro	Gln	Ile	Tyr	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	370	375	380	
	His	Thr	Ile	Glu	Glu	Trp	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asn	385	390	395	400
	Ser	Glu	Glu	Lys	Thr	Lys	Asn	Gly	Val	Val	Lys	Gly	Gln	Pro	Ser	Pro	405	410	415	
35	Ser	Ala	Gln	Val	Gln	Gln											420			

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

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5      (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "oligonucleotide"

      (iii) HYPOTHETICAL: NO

      (iv) ANTI-SENSE: NO

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
10    GAACGGCGGG CAGCCAACAT GCGGCGGCG                               30

      (2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 36 base pairs
          (B) TYPE: nucleic acid
15      (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
          (A) DESCRIPTION: /desc = "oligonucleotide"

        (iii) HYPOTHETICAL: NO

20      (iv) ANTI-SENSE: NO

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

      GGGCTCGAGC CTGACAAATT TAAGATCTGT ATCCTG                               36

      (2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 28 base pairs
          (B) TYPE: nucleic acid
25      (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: other nucleic acid
30      (A) DESCRIPTION: /desc = "oligonucleotide"

        (iii) HYPOTHETICAL: NO

        (iv) ANTI-SENSE: NO

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

      TTAACATATG GCGGCGGCGG CGGCGGCG                               28

35      (2) INFORMATION FOR SEQ ID NO:7:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 25 base pairs

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35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAAAAGCTTG TAAAGATCTG TTTCCATGAG GTCCGTTACT AT

42

(2) INFORMATION FOR SEQ ID NO:11:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

20 CAAAAGCTTG TAAAGATCTG TTTCCATGAG GTCCGCTACT AT

42

(2) INFORMATION FOR SEQ ID NO:12:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAAAAGCTTG TAAAGATCTG CTCCCATGAG GTGCGTTACT AGATATAC

48

(2) INFORMATION FOR SEQ ID NO:13:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCTTTACA AGCTTTTGAA GACACAAC

28

(2) INFORMATION FOR SEQ ID NO:14:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTGGTGTAG CCCTTGGAAT TCAACATA

28

20 (2) INFORMATION FOR SEQ ID NO:15:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

30 (ix) FEATURE:

(A) NAME/KEY: Region

(B) LOCATION: 1..6

(D) OTHER INFORMATION: /note= "C-terminal tag"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35 Glu Tyr Met Pro Met Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGGCACAC CATCACCATC ACCATCCCAA GAAGAAGCCG ACGCCCATCC AG 52

(2) INFORMATION FOR SEQ ID NO:17:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
20 (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGGATGGGC GTCGGCTTCT TCTTGGGATG GTGATGGTGA TGGTGTGC 48

25 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCTCTAGAGC TCCATGGGCA GCAAAAGCAA AGTTGACAA 39

(2) INFORMATION FOR SEQ ID NO:19:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO
- 10 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGCGGATCC TCATTCTGAA TTCATTACTT CCTTGTA

37

(2) INFORMATION FOR SEQ ID NO:20:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
20 (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAAGATGTT TACTTAGTAG CGGAACTGAT GGATGCCAA

39

25 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAAGATGTTT ACTTAGTAAC GGGACTGATG GATGCCAAC

39

(2) INFORMATION FOR SEQ ID NO:22:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTAATGGAAC TGATGGGTGC CAACTTATGT CAAGTG

36

(2) INFORMATION FOR SEQ ID NO:23:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "EGF receptor peptide"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Arg Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn
 1 5 10 15
 Gln Ala Leu Leu Arg
 20

30 (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	Met	Ser	Ser	Pro	Pro	Thr	Arg	Ser	Gly	Phe	Tyr	Arg	Gln	Glu	Val	
	1				5					10					15	
	Thr	Lys	Thr	Ala	Trp	Glu	Val	Arg	Ala	Val	Tyr	Arg	Asp	Leu	Gln	Pro
				20					25					30		
5	Val	Gly	Ser	Gly	Ala	Tyr	Gly	Ala	Val	Cys	Ser	Ala	Val	Asp	Gly	Arg
			35					40					45			
	Thr	Gly	Ala	Lys	Val	Ala	Ile	Lys	Lys	Leu	Tyr	Arg	Pro	Phe	Gln	Ser
		50					55					60				
10	Glu	Leu	Phe	Ala	Lys	Leu	Ala	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His
	65					70					75					80
	Met	Arg	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Asp
					85					90					95	
	Glu	Thr	Leu	Asp	Asp	Phe	Thr	Asp	Phe	Tyr	Leu	Val	Met	Pro	Phe	Met
				100					105					110		
15	Gly	Thr	Asp	Leu	Gly	Lys	Leu	Met	Lys	His	Glu	Lys	Leu	Gly	Glu	Asp
			115					120					125			
	Arg	Ile	Gln	Phe	Leu	Val	Tyr	Gln	Met	Met	Lys	Gly	Leu	Arg	Tyr	Ile
		130					135					140				
20	His	Ala	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Leu	Ala
	145					150					155					160
	Val	Asn	Glu	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg
					165					170					175	
	Gln	Ala	Asp	Ser	Glu	Met	Thr	Gly	Tyr	Val	Val	Thr	Arg	Trp	Tyr	Arg
				180					185					190		
25	Ala	Pro	Glu	Val	Ile	Leu	Asn	Trp	Ile	Ala	Tyr	Thr	Gln	Thr	Val	Asp
			195					200					205			
	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Ile	Thr	Gly	Lys	Thr
		210					215					220				
30	Leu	Phe	Lys	Gly	Ser	Asp	His	Leu	Asp	Gln	Leu	Lys	Glu	Ile	Met	Lys
	225					230					235					240
	Val	Thr	Gly	Thr	Pro	Pro	Ala	Glu	Phe	Val	Gln	Arg	Leu	Gln	Ser	Asp
					245					250					255	
	Glu	Ala	Lys	Asn	Tyr	Met	Lys	Gly	Leu	Pro	Glu	Leu	Glu	Lys	Lys	Asp
				260					265					270		
35	Phe	Ala	Ser	Ile	Leu	Thr	Asn	Ala	Ser	Pro	Leu	Ala	Val	Asn	Leu	Leu

Pro Pro Arg Gln Leu Gly Ala Arg Val Ser Lys Glu Thr Pro Leu
355 360 365

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr
165 170 175

Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp
160 185 190

Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg
195 200 205

5 Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys
210 215 220

Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser
225 230 235 240

10 Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His
245 250 255

Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile
260 265 270

Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr
275 280 285

15 Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu
290 295 300

Asp Leu Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr
305 310 315 320

20 Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro
325 330 335

Thr Asp Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu
340 345 350

Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr
355 360 365

25 Ala Arg Phe Gln Pro Gly Val Leu Glu Ala Pro
370 375

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

35 Met Ser Leu Ile Arg Lys Lys Gly Phe Tyr Lys Gln Glu Leu Asn Lys
1 5 10 15

Thr Ala Trp Glu Leu Pro Lys Thr Tyr Val Ser Pro Thr His Val Gly
20 25 30

	Ser	Gly	Ala	Tyr	Gly	Ser	Trp	Cys	Ser	Ala	Ile	Asp	Lys	Arg	Ser	Gly	
			35					40					45				
	Glu	Lys	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Glu	Ile	
		50					55					60					
5	Phe	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Leu	Leu	Leu	Lys	His	Met	Gln	
	65					70					75					80	
	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Ser	Ser	
					85					90					95		
10	Leu	Arg	Asn	Phe	Tyr	Asp	Phe	Tyr	Leu	Val	Met	Pro	Phe	Met	Gln	Thr	
				100						105					110		
	Asp	Leu	Gln	Lys	Ile	Met	Gly	Met	Glu	Phe	Ser	Glu	Glu	Lys	Ile	Gln	
			115					120					125				
	Tyr	Leu	Val	Tyr	Gln	Met	Leu	Lys	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	
		130					135						140				
15	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Leu	Ala	Val	Asn	Glu	
	145					150					155					160	
	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Ala	Asp	
					165					170					175		
20	Ala	Glu	Met	Thr	Gly	Tyr	Val	Val	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	
				180						185					190		
	Val	Ile	Leu	Ser	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser	
			195					200					205				
	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Leu	Thr	Gly	Lys	Thr	Leu	Phe	Lys	
		210					215					220					
25	Gly	Lys	Asp	Tyr	Leu	Asp	Gln	Leu	Thr	Gln	Ile	Leu	Lys	Val	Thr	Gly	
	225					230					235					240	
	Val	Pro	Gly	Thr	Glu	Phe	Val	Gln	Lys	Leu	Asn	Asp	Lys	Ala	Ala	Lys	
					245					250					255		
30	Ser	Tyr	Ile	Gln	Ser	Leu	Pro	Gln	Thr	Pro	Arg	Lys	Asp	Phe	Thr	Gln	
				260					265					270			
	Leu	Phe	Pro	Arg	Ala	Ser	Pro	Gln	Ala	Ala	Asp	Leu	Leu	Glu	Lys	Met	
			275					280					285				
	Leu	Glu	Leu	Asp	Val	Asp	Lys	Arg	Leu	Thr	Ala	Ala	Gln	Ala	Leu	Thr	
		290					295					300					
35	His	Pro	Phe	Phe	Glu	Pro	Phe	Arg	Asp	Pro	Glu	Glu	Glu	Thr	Glu	Ala	
	305					310					315					320	
	Gln	Gln	Pro	Phe	Asp	Asp	Ser	Leu	Glu	His	Glu	Lys	Leu	Thr	Val	Asp	
					325					330					335		

003760-64/24/50

Ala Arg Lys Asp Ser Arg Arg Arg Ser Gly Met Lys Leu
355 360 365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

	Met	Ser	Leu	Ile	Arg	Lys	Lys	Gly	Phe	Tyr	Lys	Gln	Asp	Val	Asn	Lys
	1					5										15
15	Thr	Ala	Trp	Glu	Leu	Pro	Lys	Thr	Tyr	Val	Ser	Pro	Thr	His	Val	Gly
				20					25					30		
	Ser	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ser	Ala	Ile	Asp	Lys	Arg	Ser	Gly
			35					40					45			
20	Glu	Lys	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Glu	Ile
		50					55						60			
	Phe	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Leu	Leu	Leu	Lys	His	Met	Gln
	65					70					75					80
	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Ser	Ser
					85					90					95	
25	Leu	Arg	Asn	Phe	Tyr	Asp	Phe	Tyr	Leu	Val	Met	Pro	Phe	Met	Gln	Thr
				100					105					110		
	Asp	Leu	Gln	Lys	Ile	Met	Gly	Met	Glu	Phe	Ser	Glu	Glu	Lys	Ile	Gln
			115					120					125			
30	Tyr	Leu	Val	Tyr	Gln	Met	Leu	Lys	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala
		130					135						140			
	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Leu	Ala	Val	Asn	Glu
	145					150					155					160
	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Ala	Asp
					165					170					175	
35	Ala	Glu	Met	Thr	Gly	Tyr	Val	Val	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu
				180					185					190		
	Val	Ile	Leu	Ser	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser
			195					200					205			

Val Gly Cys Ile Met Ala Glu Met Leu Thr Gly Lys Thr Leu Phe Lys
210 215 220

Gly Lys Asp Tyr Leu Asp Gln Leu Thr Gln Ile Leu Lys Val Thr Gly
225 230 235 240

5 Val Pro Gly Thr Glu Phe Val Gln Lys Leu Asn Asp Lys Ala Ala Lys
245 250 255

Ser Tyr Ile Gln Ser Leu Pro Gln Thr Pro Arg Lys Asp Phe Thr Gln
260 265 270

10 Leu Phe Pro Arg Ala Ser Pro Gln Ala Ala Asp Leu Leu Glu Lys Met
275 280 285

Leu Glu Leu Asp Val Asp Lys Arg Leu Thr Ala Ala Gln Ala Leu Thr
290 295 300

His Pro Phe Phe Glu Pro Phe Arg Asp Pro Glu Glu Glu Thr Glu Ala
305 310 315 320

15 Gln Gln Pro Phe Asp Asp Ser Leu Glu His Glu Lys Leu Thr Val Asp
325 330 335

Glu Trp Lys Gln His Ile Tyr Lys Glu Ile Val Asn Phe Ser Pro Ile
340 345 350

20 Ala Arg Lys Asp Ser Arg Arg Arg Ser Gly Met Lys Leu
355 360 365

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30 Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val
1 5 10 15

Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr
20 25 30

Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe
35 40 45

35 Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr
50 55 60

Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala
65 70 75 80

	Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser	85	90	95
	Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu	100	105	110
5	Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn	115	120	125
	Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu	130	135	140
10	Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu	145	150	155
	Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly	165	170	175
	Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro	180	185	190
15	Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe	195	200	205
	Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val	210	215	220
20	Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr	225	230	235
	Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met	245	250	255
	Val Arg His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp	260	265	270
25	Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys	275	280	285
	Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr	290	295	300
30	Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala	305	310	315
	Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu	325	330	335
	Ser Lys Met Leu Val Ile Asp Pro Ala Lys Arg Ile Ser Val Asp Asp	340	345	350
35	Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val	355	360	365
	Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu	370	375	380

Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro
405 410 415

5 Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
 420 425 430

Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp
435 440 445

Thr Asp Ser Ser Leu Glu Ala Ser Ala Gly Pro Leu Gly Cys Cys Arg
10 450 455 460

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ser Asp Ser Lys Cys Asp Ser Gln Phe Tyr Ser Val Gln Val Ala
20 1 5 10 15

Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Gln Leu Lys Pro Ile
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Phe Asp Thr Val Leu
35 40 45

25 Gly Ile Ser Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Leu Lys Cys Val
65 70 75 80

30 Asn His Lys Asn Ile Ile Ser Leu Leu Asn Val Phe Thr Pro Gln Lys
85 90 95

Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met Glu Leu Met Asp
100 105 110

Ala Asn Leu Cys Gln Val Ile His Met Glu Leu Asp His Glu Arg Met
115 120 125

35 Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser
130 135 140

Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys
145 150 155 160

	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	
					165					170					175		
	Cys	Asn	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
				180					185					190			
5	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile	
			195					200					205				
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Leu	Val	Lys	Gly	Cys	Val	Ile	
			210				215						220				
10	Phe	Gln	Gly	Thr	Asp	His	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
						230					235					240	
	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
						245				250					255		
	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu	
				260					265					270			
15	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys	
			275					280					285				
	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
			290				295					300					
20	Asp	Pro	Asp	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Arg	His	Pro	Tyr	
		305				310					315					320	
	Ile	Thr	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Gln	
					325					330					335		
	Ile	Tyr	Asp	Ala	Gln	Leu	Glu	Glu	Arg	Glu	His	Ala	Ile	Glu	Glu	Trp	
				340					345					350			
25	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Trp	Glu	Glu	Arg	Ser	Lys	
			355					360					365				
	Asn	Gly	Val	Val	Lys	Asp	Gln	Pro	Ser	Ala	Gln	Met	Gln	Gln			
			370				375					380					

(2) INFORMATION FOR SEQ ID NO:30:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Ser	Asp	Ser	Lys	Cys	Asp	Ser	Gln	Phe	Tyr	Ser	Val	Gln	Val	Ala
1				5					10					15	

	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Gln	Leu	Lys	Pro	Ile
				20					25					30		
	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Phe	Asp	Thr	Val	Leu
			35					40					45			
5	Gly	Ile	Ser	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln
		50					55					60				
	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Leu	Lys	Cys	Val
	65					70					75					80
10	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys
				85						90					95	
	Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu	Val	Met	Glu	Leu	Met	Asp
				100					105					110		
	Ala	Asn	Leu	Cys	Gln	Val	Ile	His	Met	Glu	Leu	Asp	His	Glu	Arg	Met
			115					120					125			
15	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser
		130					135					140				
	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys
	145					150					155					160
20	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala
					165					170					175	
	Cys	Thr	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg
				180					185					190		
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile
			195					200					205			
25	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Val	Leu	His	Lys	Val	Leu
		210					215					220				
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln
	225					230					235					240
30	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val
					245					250					255	
	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu
				260					265					270		
	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys
			275					280					285			
35	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile
		290					295					300				
	Asp	Pro	Asp	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Arg	His	Pro	Tyr
	305					310					315					320

Ile Thr Val Trp Tyr Asp Pro Ala Glu Ala Glu Ala Pro Pro Pro Gln
325 330 335

Ile Tyr Asp Ala Gln Leu Glu Glu Arg Glu His Ala Ile Glu Glu Trp
340 345 350

5 Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Trp Glu Glu Arg Ser Lys
355 360 365

Asn Gly Val Val Lys Asp Gln Pro Ser Ala Gln Met Gln Gln
370 375 380

(2) INFORMATION FOR SEQ ID NO:31:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ser Asp Ser Lys Cys Asp Ser Gln Phe Tyr Ser Val Gln Val Ala
1 5 10 15

20 Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Gln Leu Lys Pro Ile
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Phe Asp Thr Val Leu
35 40 45

Gly Ile Ser Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

25 Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Leu Lys Cys Val
65 70 75 80

Asn His Lys Asn Ile Ile Ser Leu Leu Asn Val Phe Thr Pro Gln Lys
85 90 95

30 Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met Glu Leu Met Asp
100 105 110

Ala Asn Leu Cys Gln Val Ile His Met Glu Leu Asp His Glu Arg Met
115 120 125

Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser
130 135 140

35 Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys
145 150 155 160

Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala
165 170 175

	Cys	Thr	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
				180					185					190			
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile	
			195					200					205				
5	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Val	Leu	His	Lys	Val	Leu	
		210					215					220					
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
	225					230					235					240	
10	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
					245					250					255		
	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu	
				260					265					270			
	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys	
			275					280					285				
15	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
		290					295					300					
	Asp	Pro	Asp	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Arg	His	Pro	Tyr	
	305					310					315					320	
20	Ile	Thr	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Gln	
					325					330					335		
	Ile	Tyr	Asp	Ala	Gln	Leu	Glu	Glu	Arg	Glu	His	Ala	Ile	Glu	Glu	Trp	
				340					345					350			
	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Trp	Glu	Glu	Arg	Ser	Lys	
			355					360					365				
25	Asn	Gly	Val	Val	Lys	Asp	Gln	Pro	Ser	Asp	Ala	Ala	Val	Ser	Ser	Asn	
		370					375					380					
	Ala	Thr	Pro	Ser	Gln	Ser	Ser	Ser	Ile	Asn	Asp	Ile	Ser	Ser	Met	Ser	
	385					390					395					400	
30	Thr	Glu	Gln	Thr	Leu	Ala	Ser	Asp	Thr	Asp	Ser	Ser	Leu	Asp	Ala	Ser	
					405					410					415		
	Thr	Gly	Pro	Leu	Glu	Gly	Cys	Arg									
					420												

(2) INFORMATION FOR SEQ ID NO:32:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 424 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

	Met	Ser	Asp	Ser	Lys	Cys	Asp	Ser	Gln	Phe	Tyr	Ser	Val	Gln	Val	Ala	
	1				5					10					15		
5	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Gln	Leu	Lys	Pro	Ile	
				20					25					30			
	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Phe	Asp	Thr	Val	Leu	
			35					40					45				
	Gly	Ile	Asn	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	
		50					55					60					
10	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Leu	Lys	Cys	Val	
	65					70					75					80	
	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys	
				85						90					95		
15	Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu	Val	Met	Glu	Leu	Met	Asp	
				100					105					110			
	Ala	Asn	Leu	Cys	Gln	Val	Ile	His	Met	Glu	Leu	Asp	His	Glu	Arg	Met	
			115					120					125				
	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	
		130					135					140					
20	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	
	145					150					155					160	
	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	
				165						170					175		
25	Cys	Thr	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
			180						185					190			
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile	
			195					200					205				
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Leu	Val	Lys	Gly	Cys	Val	Ile	
		210					215					220					
30	Phe	Gln	Gly	Thr	Asp	His	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
	225					230					235					240	
	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
				245						250					255		
35	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu	
			260						265					270			
	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys	
			275					280					285				
	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
		290					295						300				

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ser	Arg	Ser	Lys	Arg	Asp	Asn	Asn	Phe	Tyr	Ser	Val	Glu	Ile	Gly	
1				5					10					15		
Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Asn	Leu	Lys	Pro	Ile	
			20					25					30			
Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Tyr	Asp	Ala	Ile	Leu	
		35					40					45				
Glu	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	
	50					55					60					
Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Met	Lys	Cys	Val	
65					70					75					80	
Asn	His	Lys	Asn	Ile	Ile	Gly	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys	
			85						90					95		
Ser	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp	
			100					105					110			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5	Met	Ser	Arg	Ser	Lys	Arg	Asp	Asn	Asn	Phe	Tyr	Ser	Val	Glu	Ile	Gly	1	5	10	15
	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Asn	Leu	Lys	Pro	Ile	20	25	30	
	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Tyr	Asp	Ala	Ile	Leu	35	40	45	
10	Glu	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	50	55	60	
	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Met	Lys	Cys	Val	65	70	75	80
15	Asn	His	Lys	Asn	Ile	Ile	Gly	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys	85	90	95	
	Ser	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp	100	105	110	
	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met	115	120	125	
20	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	130	135	140	
	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	145	150	155	160
25	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	165	170	175	
	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	180	185	190	
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu	195	200	205	
30	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu	210	215	220	
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	225	230	235	240
35	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	245	250	255	
	Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu	260	265	270	

Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys
275 280 285

Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile
290 295 300

5 Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr
305 310 315 320

Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys
325 330 335

10 Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp
340 345 350

Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Glu Arg Thr Lys
355 360 365

Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Gly Ala Ala Val Ile
370 375 380

15 Asn Gly Ser Gln His Pro Ser Ser Ser Ser Ser Val Asn Asp Val Ser
385 390 395 400

Ser Met Ser Thr Asp Pro Thr Leu Ala Ser Asp Thr Asp Ser Ser Leu
405 410 415

20 Glu Ala Ala Ala Gly Pro Leu Gly Cys Cys Arg
420 425

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

30 Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly
1 5 10 15

Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu
35 40 45

35 Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val
65 70 75 80

	Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys	85	90	95
	Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp	100	105	110
5	Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met	115	120	125
	Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser	130	135	140
10	Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys	145	150	155
	Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala	165	170	175
	Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg	180	185	190
15	Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Ile	195	200	205
	Trp Ser Val Gly Cys Ile Met Gly Glu Met Ile Lys Gly Gly Val Leu	210	215	220
20	Phe Pro Gly Thr Asp His Ile Asp Gln Trp Asn Lys Val Ile Glu Gln	225	230	235
	Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val	245	250	255
	Arg Thr Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Tyr Ser Phe Glu	260	265	270
25	Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys	275	280	285
	Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile	290	295	300
30	Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr	305	310	315
	Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys	325	330	335
	Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp	340	345	350
35	Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Glu Arg Thr Lys	355	360	365
	Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Ala Gln Val Gln Gln	370	375	380

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

10 Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly
1 5 10 15

Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu
35 40 45

15 Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val
65 70 75 80

20 Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys
85 90 95

Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp
100 105 110

Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met
115 120 125

25 Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser
130 135 140

Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys
145 150 155 160

30 Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala
165 170 175

Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg
180 185 190

Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Ile
195 200 205

35 Trp Ser Val Gly Cys Ile Met Gly Glu Met Ile Lys Gly Gly Val Leu
210 215 220

Phe Pro Gly Thr Asp His Ile Asp Gln Trp Asn Lys Val Ile Glu Gln
225 230 235 240

Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val
245 250 255

Arg Thr Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Tyr Ser Phe Glu
260 265 270

5 Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys
275 280 285

Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile
290 295 300

10 Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr
305 310 315 320

Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys
325 330 335

Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp
340 345 350

15 Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Glu Arg Thr Lys
355 360 365

Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Gly Ala Ala Val Ile
370 375 380

20 Asn Gly Ser Gln His Pro Ser Ser Ser Ser Val Asn Asp Val Ser
385 390 395 400

Ser Met Ser Thr Asp Pro Thr Leu Ala Ser Asp Thr Asp Ser Ser Leu
405 410 415

Glu Ala Ala Ala Gly Pro Leu Gly Cys Cys Arg
420 425

25 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ser Gly Pro Arg Ala Gly Phe Tyr Arg Gln Glu Leu Asn Lys Thr
1 5 10 15

35 Val Trp Glu Val Pro Gln Arg Leu Gln Gly Leu Arg Pro Val Gly Ser
20 25 30

Gly Ala Tyr Gly Ser Val Cys Ser Ala Tyr Asp Ala Arg Leu Arg Gln
35 40 45

	Lys	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Leu	Ile	His	
	50						55					60					
	Ala	Arg	Arg	Thr	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His	Leu	Lys	His	
	65					70					75					80	
5	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Thr	Ser	Ile	
					85					90					95		
	Glu	Asp	Phe	Ser	Glu	Val	Tyr	Leu	Val	Thr	Thr	Leu	Met	Gly	Ala	Asp	
				100					105					110			
10	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Ala	Leu	Ser	Asp	Glu	His	Val	Gln	
			115					120					125				
	Phe	Leu	Val	Tyr	Gln	Leu	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	
		130					135					140					
	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Val	Ala	Val	Asn	Glu	
	145					150					155					160	
15	Asp	Cys	Glu	Leu	Arg	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Gln	Ala	Asp	
					165					170					175		
	Glu	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	
				180					185					190			
20	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser	
			195					200					205				
	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Gln	Gly	Lys	Ala	Leu	Phe	Pro	
		210					215					220					
	Gly	Ser	Asp	Tyr	Ile	Asp	Gln	Leu	Lys	Arg	Ile	Met	Glu	Val	Val	Gly	
	225					230					235					240	
25	Thr	Pro	Ser	Pro	Glu	Val	Leu	Ala	Lys	Ile	Ser	Ser	Glu	His	Ala	Arg	
					245					250					255		
	Thr	Tyr	Ile	Gln	Ser	Leu	Pro	Pro	Met	Pro	Gln	Lys	Asp	Leu	Ser	Ser	
				260					265					270			
30	Ile	Phe	Arg	Gly	Ala	Asn	Pro	Leu	Ala	Ile	Asp	Leu	Leu	Gly	Arg	Met	
			275					280					285				
	Leu	Val	Leu	Asp	Ser	Asp	Gln	Arg	Val	Ser	Ala	Ala	Glu	Ala	Leu	Ala	
		290					295					300					
	His	Ala	Tyr	Phe	Ser	Gln	Tyr	His	Asp	Pro	Glu	Asp	Glu	Pro	Glu	Ala	
	305					310					315					320	
35	Glu	Pro	Tyr	Asp	Glu	Gly	Val	Glu	Ala	Lys	Glu	Arg	Thr	Leu	Glu	Glu	
					325					330					335		
	Trp	Lys	Glu	Leu	Thr	Tyr	Gln	Glu	Val	Leu	Ser	Phe	Lys	Pro	Pro	Glu	
				340					345					350			

1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2